



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/529,043B

DATE: 02/20/2002
TIME: 16:57:58

Input Set : A:\Fzj010-1.txt
Output Set: N:\CRF3\02202002\I529043B.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Forschungszentrum Juelich GmbH
6 <120> TITLE OF INVENTION: Method for microbial production of amino acids of the
7 aspartate and/or glutamate family and agents which can
8 be used in said method
10 <130> FILE REFERENCE: 1
12 <140> CURRENT APPLICATION NUMBER: 09/529,043B
13 <141> CURRENT FILING DATE: 2000-04-03
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06210
16 <151> PRIOR FILING DATE: 1998-09-30
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3728
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (165)..(3587)
30 <223> OTHER INFORMATION: pyruvate carboxylase
32 <400> SEQUENCE: 1
E--> 33 cgcaaccgtg cttgaagtctg tgcaggtcag gggagtgttg cccgaaaaca ttgagagggaa 60 format
34 60 error
E--> 36 aacaaaaacc gatgtttgat tgggggaatc gggggttacg atactaggac gcagtgaactg 120
37 120 ↓
E--> 39 ctatcacccct tggcggtctc ttgttcaaag gaataattac tcta gtg tcg act cac
40 176 Val Ser Thr His
41 1
42
E--> 44 aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc
45 224
46 Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg
47 5 10 15 20
E--> 49 ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca
50 272
51 Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala
52 25 30 35
E--> 54 gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc
55 320
56 Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg

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57 40 45 50
E--> 59 tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc.
60 368
61 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val
62 55 60 65
E--> 64 aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt
65 416
66 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val
67 70 75 80
E--> 69 aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc
70 464
71 Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala
72 85 90 95 100
E--> 74 cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca
75 512
76 Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro
77 105 110 115
E--> 79 acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc
80 560
81 Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr
82 120 125 130
E--> 84 gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc
85 608
86 Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser
87 135 140 145
E--> 89 aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc
90 656
91 Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro
92 150 155 160
E--> 94 atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt
95 704
96 Ile Phe Val Lys Ala Val Ala Gly Gly Gly Arg Gly Met Arg Phe
97 165 170 175 180
E--> 99 gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt
100 752
101 Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg
102 185 190 195
E--> 104 gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct
105 800
106 Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala
107 200 205 210
E--> 109 gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act
110 848
111 Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr
112 215 220 225
E--> 114 gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt
115 896
116 Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg
117 230 235 240

*same
error*

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E--> 119 cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa
 120 944
 121 His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu
 122 245 250 255 260
 E--> 124 ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att
 125 992
 126 Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile
 127 265 270 275
 E--> 129 ggt tac cag ggc gcg gga acc gtt gaa ttc ttg gtc gat gaa aag ggc
 130 1040
 131 Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly
 132 280 285 290
 E--> 134 aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc
 135 1088
 136 Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr
 137 295 300 305
 E--> 139 gtt act gaa gaa gtc acc gag gtt gac ctg gtt aag gcg cag atg cgc
 140 1136
 141 Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg
 142 310 315 320
 E--> 144 ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag
 145 1184
 146 Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys
 147 325 330 335 340
 E--> 149 atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat
 150 1232
 151 Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp
 152 345 350 355
 E--> 154 cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc
 155 1280
 156 Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg
 157 360 365 370
 E--> 159 tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt
 160 1328
 161 Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly
 162 375 380 385
 E--> 164 ggc gaa atc acc gca cac ttt gac tcc atg ctg gtt aaa atg acc tgc
 165 1376
 166 Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys
 167 390 395 400
 E--> 169 cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg
 170 1424
 171 Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu
 172 405 410 415 420
 E--> 174 gct gag ttc acc gtc tct ggt gtt gca acc aac att ggt ttc ttg cgt
 175 1472
 176 Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg
 177 425 430 435
 E--> 179 gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga

done

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180 1520
 181 Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly
 182 440 445 450
E--> 184 ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat
 185 1568
 186 Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp
 187 455 460 465
E--> 189 gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag
 190 1616
 191 Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys
 192 470 475 480
E--> 194 cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg
 195 1664
 196 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
 197 485 490 495 500
E--> 199 cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc ctg
 200 1712
 201 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg Leu
 202 505 510 515
E--> 204 aag cag ctt ggc cca gcc gcg ttt gct cgt gat ctc cgt gag cag gac
 205 1760
 206 Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu Arg Glu Gln Asp
 207 520 525 530
E--> 209 gca ctg gca gtt act gat acc acc ttc cgc gat gca cac cag tct ttg
 210 1808
 211 Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
 212 535 540 545
E--> 214 ctt gcg acc cga gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc
 215 1856
 216 Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala
 217 550 555 560
E--> 219 gtc gca aag ctg act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc
 220 1904
 221 Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
 222 565 570 575 580
E--> 224 gcg acc tac gat gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac
 225 1952
 226 Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp
 227 585 590 595
E--> 229 agg ctc gac gag ctg cgc gag gcg atg ccg aat gta aac att cag atg
 230 2000
 231 Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met
 232 600 605 610
E--> 234 ctg ctt cgc ggc cgc aac acc gtg gga tac acc ccg tac cca gac tcc
 235 2048
 236 Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser
 237 615 620 625
E--> 239 gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc
 240 2096

parse

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241 Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile
242 630 635 640
E--> 244 ttc cgc atc ttc gac gcg ctt aac gac gtc tcc cag atg cgt cca gca
245 2144
246 Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala
247 645 650 655 660
E--> 249 atc gac gca gtc ctg gag acc aac acc gcg gta gcc gag gtg gct atg
250 2192
251 Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met
252 665 670 675
E--> 254 gct tat tct ggt gat ctc tct gat cca aat gaa aag ctc tac acc ctg
255 2240
256 Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu
257 680 685 690
E--> 259 gat tac tac cta aag atg gca gag gag atc gtc aag tct ggc gct cac
260 2288
261 Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His
262 695 700 705
E--> 264 atc ttg gcc att aag gat atg gct ggt ctg ctt cgc cca gct gcg gta
265 2336
266 Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val
267 710 715 720
E--> 269 acc aag ctg gtc acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac
270 2384
271 Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His
272 725 730 735 740
E--> 274 gtg cac acc cac gac act gcg ggt ggc cag ctg gca acc tac ttt gct
275 2432
276 Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala
277 745 750 755
E--> 279 gca gct caa gct ggt gca gat gct gtt gac ggt gct tcc gca cca ctg
280 2480
281 Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
282 760 765 770
E--> 284 tct ggc acc acc tcc cag cca tcc ctg tct gcc att gtt gct gca ttc
285 2528
286 Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
287 775 780 785
E--> 289 gcg cac acc cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac
290 2576
291 Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp
292 790 795 800
E--> 294 ctc gag ccg tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag
295 2624
296 Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu
297 805 810 815 820
E--> 299 tct gga acc cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca
300 2672
301 Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro

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302 825 830 835
E--> 304 ggc gga cag ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt
 305 2720
 306 Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu
 307 840 845 850
E--> 309 gcg gat cgt ttc gaa ctc atc gaa gac aac tac gca gcc gtt aat gag
 310 2768
 311 Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ala Val Asn Glu
 312 855 860 865
E--> 314 atg ctg gga cgc cca acc aag gtc acc cca tcc tcc aag gtt gtt ggc
 315 2816
 316 Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
 317 870 875 880
E--> 319 gac ctc gca ctc cac ctc gtt ggt gcg ggt gtg gat cca gca gac ttt
 320 2864
 321 Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 322 885 890 895 900
E--> 324 gct gcc gat cca caa aag tac gac atc cca gac tct gtc atc gcg ttc
 325 2912
 326 Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 327 905 910 915
E--> 329 ctg cgc ggc gag ctt ggt aac cct cca ggt ggc tgg cca gag cca ctg
 330 2960
 331 Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 332 920 925 930
E--> 334 cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc aag gca cct ctg acg
 335 3008
 336 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 337 935 940 945
E--> 339 gaa gtt cct gag gaa gag cag gcg cac ctc gac gct gat gat tcc aag
 340 3056
 341 Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 342 950 955 960
E--> 344 gaa cgt cgc aat agc ctc aac cgc ctg ctg ttc ccg aag cca acc gaa
 345 3104
 346 Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 347 965 970 975 980
E--> 349 gag ttc ctc gag cac cgt cgc cgc ttc ggc aac acc tct gcg ctg gat
 350 3152
 351 Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 352 985 990 995
E--> 354 gat cgt gaa ttc ttc tac ggc ctg gtc gaa ggc cgc gag act ttg atc
 355 3200
 356 Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 357 1000 1005 1010
E--> 359 cgc ctg cca gat gtg cgc acc cca ctg ctt gtt cgc ctg gat gcg atc
 360 3248
 361 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 362 1015 1020 1025

Same

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E--> 364 tct gag cca gac gat aag ggt atg cgc aat gtt gtg gcc aac gtc aac
365 3296
366 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
367 1030 1035 1040
E--> 369 ggc cag atc cgc cca atg cgt gtg cgt gac cgc tcc gtt gag tct gtc
370 3344
371 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
372 1045 1050 1055 1060
E--> 374 acc gca acc gca gaa aag gca gat tcc tcc aac aag ggc cat gtt gct
375 3392
376 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
377 1065 1070 1075
E--> 379 gca cca ttc gct ggt gtt gtc acc gtg act gtt gct gaa ggt gat gag
380 3440
381 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
382 1080 1085 1090
E--> 384 gtc aag gct gga gat gca gtc gca atc atc gag gct atg aag atg gaa
385 3488
386 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
387 1095 1100 1105
E--> 389 gca aca atc act gct tct gtt gac ggc aaa atc gat cgc gtt gtg gtt
390 3536
391 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
392 1110 1115 1120
E--> 394 cct gct gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc
395 3584
396 Pro Ala Ala Thr Lys Val Glu Gly Asp Leu Ile Val Val Val Ser
397 1125 1130 1135 1140
E--> 399 taa acctttctgt aaaaagcccc gcgtttcct catggaggag gcggggcttt
400 3637
E--> 403 ttggggccaag atgggagatg ggtgagttgg atttggtctg attcgacact tttaaggca
404 3697
E--> 406 gagatttgaa gatggagacc aaggctaaaa g
407 3728
563 <210> SEQ ID NO: 3
564 <211> LENGTH: 19
565 <212> TYPE: DNA
566 <213> ORGANISM: Artificial Sequence
568 <220> FEATURE:
569 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
571 <400> SEQUENCE: 3
E--> 572 cgtcttcatc gaaatgaac
573 19
576 <210> SEQ ID NO: 4
577 <211> LENGTH: 19
578 <212> TYPE: DNA
579 <213> ORGANISM: Artificial Sequence
581 <220> FEATURE:
582 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer

Dane

Dane

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584 <400> SEQUENCE: 4

E--> 585 acgggtggta tccggcact

586 19

panel

VERIFICATION SUMMARY DATE: 02/20/2002
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Input Set : A:\Fzj010~1.txt
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L:33 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:572 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:3
L:585 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:4